

BLASTP 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1080938838-2992-100313990365.BLASTQ3

Query=

(362 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

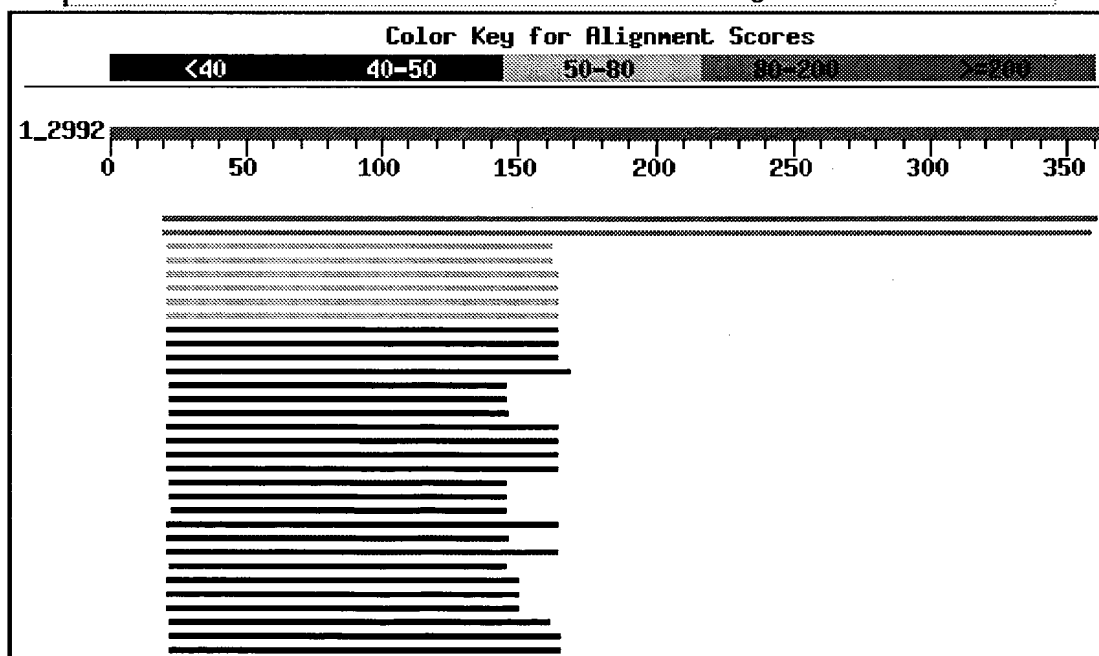
2,727,393 sequences; 760,540,814 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 32 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Score E

Sequences producing significant alignments:

(bits) Value

gi 1486493 gb AAC55101.1 	glycoprotein I	636	0.0
gi 38638266 ref NP_944449.1 	glycoprotein I [Psittacid herp...	89	1e-16
gi 12657848 gb AAK01055.1 	ORF67 [Human herpesvirus 3] >gi ...	56	1e-06
gi 9625941 ref NP_040189.1 	membrane glycoprotein I [Human ...	56	1e-06
gi 3724277 dbj BAA33764.1 	glycoprotein I [Canine herpesvirus]	51	3e-05
gi 2337933 gb AAB67059.1 	cUS7 [Canine herpesvirus] >gi 372...	50	8e-05
gi 3777490 gb AAC67213.1 	gI [Canine herpesvirus]	50	8e-05
gi 15216212 emb CAC51466.1 	glycoprotein I [Phocid herpesvi...	50	9e-05
gi 632872 gb AAB30981.1 	glycoprotein gI [Feline herpesviru...	49	2e-04
gi 893371 dbj BAA44952.1 	homologue of HSV-1 gI [Feline her...	49	2e-04
gi 1405557 emb CAA67077.1 	gI [Feline herpesvirus 1]	49	3e-04
gi 13242461 ref NP_077481.1 	glycoprotein I [Cercopithecine...	46	0.001
gi 227760 prf 1710264F	ORF 6	46	0.001
gi 10180781 gb AAG14269.1 	US7 membrane glycoprotein I-like...	45	0.002
gi 12084907 ref NP_073377.1 	US7 membrane glycoprotein I [M...	45	0.003
gi 765053 gb AAA64968.1 	membrane glycoprotein I >gi 226549...	45	0.004
gi 42795204 gb AAS45961.1 	envelope glycoprotein I [Equine ...	45	0.004
gi 9626810 ref NP_041082.1 	membrane glycoprotein I [Equine...	45	0.004
gi 40787939 ref NP_954960.1 	US7 glycoprotein I [Bovine her...	45	0.004
gi 42566423 gb AAS21042.1 	glycoprotein I [Bovine herpesvir...	45	0.004
gi 22654930 gb AAM97725.1 	glycoprotein I [Gallid herpesvir...	44	0.006
gi 22654932 gb AAM97726.1 	glycoprotein I [Gallid herpesvir...	44	0.007
gi 9629803 ref NP_045290.1 	73 [Equine herpesvirus 4] >gi 1...	43	0.009
gi 625559 pir A61162	glycoprotein I - equine herpesvirus 1...	43	0.013
gi 2924616 dbj BAA25021.1 	glycoprotein I homologue [Equine...	42	0.022
gi 22654928 gb AAM97724.1 	glycoprotein I [Gallid herpesvir...	41	0.043
gi 10834952 ref NP_066913.1 	glycoprotein I [Gallid herpesv...	39	0.19
gi 138330 sp P07646 VGLI PRVRI	GLYCOPROTEIN GP63 PRECURSOR ...	39	0.21
gi 40254013 tpg DAA02208.1 	TPA: membrane glycoprotein gI p...	39	0.21
gi 37576286 gb AAQ86799.1 	membrane glycoprotein gI [Suid h...	39	0.21
gi 9629887 ref NP_045371.1 	glycoprotein I [Bovine herpesvi...	37	0.78
gi 1174955 sp Q08102 VGLI BHV1S	Glycoprotein I >gi 420427 p...	37	1.0

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|1486493|gb|AAC55101.1| glycoprotein I

Length = 362

Score = 636 bits (1641), Expect = 0.0

Identities = 319/342 (93%), Positives = 319/342 (93%)

Query: 21 MGIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITN 80

MGIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITN

Sbjct: 21 MGIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITN 80

Query: 81 QCYQELSEERFENCTHRSSSVFVGCKVTEYTFASNRLTGPPHPFKLTIRNPRPNDSGMF 140

QCYQELSEERFENCTHRSSSVFVGCKVTEYTFASNRLTGPPHPFKLTIRNPRPNDSGMF

Sbjct: 81 QCYQELSEERFENCTHRSSSVFVGCKVTEYTFASNRLTGPPHPFKLTIRNPRPNDSGMF 140

Query: 141 YVIVRLDDTKEPIDVFQAIQLSVYQFANTAATRGLYSKASCRTFGLPTVQLEAYLRTEESW 200

YVIVRLDDTKEPIDVFQAIQLSVYQFANTAATRGLYSKASCRTFGLPTVQLEAYLRTEESW

Sbjct: 141 YVIVRLDDTKEPIDVFQAIQLSVYQFANTAATRGLYSKASCRTFGLPTVQLEAYLRTEESW 200

Query: 201 RNWQAYXXXXXXXXXXXXXXXXXXXXXSELEAEHFTFPWLENGVDHYEPTPANENSNV 260
 RNWQAY SELEAEHFTFPWLENGVDHYEPTPANENSNV
 Sbjct: 201 RNWQAYVATEATTTSAEATTPTPTVATSAEAEHFTFPWLENGVDHYEPTPANENSNV 260

Query: 261 TVRLGTMSPTLIGVTVAAVVSATIGLVIVISIVTRNMCTPHRKLDTVSQDDEERSQTRRE 320
 TVRLGTMSPTLIGVTVAAVVSATIGLVIVISIVTRNMCTPHRKLDTVSQDDEERSQTRRE
 Sbjct: 261 TVRLGTMSPTLIGVTVAAVVSATIGLVIVISIVTRNMCTPHRKLDTVSQDDEERSQTRRE 320

Query: 321 SRKFGPMVACEINKGADQDSELVELVAIVNPSALSSPDSIKM 362
 SRKFGPMVACEINKGADQDSELVELVAIVNPSALSSPDSIKM
 Sbjct: 321 SRKFGPMVACEINKGADQDSELVELVAIVNPSALSSPDSIKM 362

☐ >gi|38638266|ref|NP_944449.1| glycoprotein I [Psittacid herpesvirus 1]
 gi|34500272|gb|AAQ73755.1| glycoprotein I [Psittacid herpesvirus 1]
 Length = 408

Score = 89.4 bits (220), Expect = 1e-16
 Identities = 103/386 (26%), Positives = 150/386 (38%), Gaps = 58/386 (15%)

Query: 21 MGIVITGNHVSARIDDDHIVIVAPREATIQLQLFFMPGQRPHPYSGTVRVAFRSDITN 80
 +G VI G VS +D +V E + +L F+ QRP PY GTVRV F+ +
 Sbjct: 22 LGTVIKGLGVSGVFEDTLVVFEKVETE-DVGARLVFLGDQRPKNPYGGTVRVLFQPGESG 80

Query: 81 QCYQELSEERFENCTHRSSSVFVGCKVTEYTFSA--SNRLTGPPHPFKLTIRNPRPND SG 138
 C L + R+ NCT+ S++VF GC T+ FS +NR T P +++R P DSG
 Sbjct: 81 TCSIPLLQVRYSNCTNTSAAVFSGCYRTDTEFSVPRANRGTS PGF---VSLRTPTMLDSG 137

Query: 139 MFYVIVRLDDTKEPIDVFAIQ-LSVYQFANT-----AATRGLYSKAS----- 179
 YV V LD P D F I+ +S+Y T R Y AS
 Sbjct: 138 DIYVTVHLDHLPRP-DAFRIKFVSLYTGNETVRISTKDRAGRDRDSYGGASSPVGGGRDSN 196

Query: 180 -----CRTFGLPTVQLEAYLRTEESWRNWQA-YXXXXXXXXXXXXXXXXX 219
 CR G L YL TEESW W + +
 Sbjct: 197 RRTASRNDDGDLPLALYGPCRPGCKNCKNLREYLLTEESWHEWTSVFAPTTVAPT TTVAT 256

Query: 220 XXXXXXXXXXXXSELEAEHFTFPWLENGVDHYEP--TPANENSNVTVRLGTMS---PTLIGV 274
 + + AE T G EP T + N+T S P L +
 Sbjct: 257 TAMRSTTVSFATMTAEVIT----STGTVSMEPHNTTTADMVNLTAA PPPSEPVPALNAL 312

Query: 275 TVAAVVSATIGLVIVISIVTRNMCTPHRKLDTVSQDDEERSQTRRESRKFGPMVACEINK 334
 + VV T+ ++ +S++ + ++ RS + RE P + E +
 Sbjct: 313 AIGLVVGGTVASLVFLSVILGGL-ISCCARRRSARLLTRSNSAREMEDLAP--SSEDAR 369

Query: 335 GADQDSELVELVAIVNPSALSSPDSI 360
 + ++VEL +VN + LS + I
 Sbjct: 370 TSRMSPDVVELSELVNGAPLSHRNDI 395

☐ >gi|12657848|gb|AAK01055.1| ORF67 [Human herpesvirus 3]
 gi|13345201|gb|AAK19249.1| ORF67 [Human herpesvirus 3 VZV-32]
 Length = 354

Score = 56.2 bits (134), Expect = 1e-06
 Identities = 41/149 (27%), Positives = 72/149 (48%), Gaps = 9/149 (6%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPE---ATIQLQLFFMPGQRP HKP-YS GTVRVAFRSD 77
 ++ G+HVS +++ I+ P I+ QL F+ Q P YSGT+ + + +D
 Sbjct: 20 ALIFKGDHVS LQVNSSLTSILIPMQNDNYTEIKGQLVF IGEQLPTGTNYS GTLELLY-AD 78

Query: 78 ITNQCYQELSEERFENC THRSSSVFVGCKVTE---YTFSASNRLTGPPHPFKLTIRNPRP 134
 C++ + R++ C +S F+ C+ Y S T P L I P
 Sbjct: 79 TVAFCFRSVQVIRYDGCPRIRTSAFISCRYKHSWHYGNSTDRISTEPDAGV MLKITKPGI 138

Query: 135 NDSGMFYVIVRLDDTKEPIDVF AIQLSVY 163
 ND+G++ ++VRLD ++ D F + ++VY
 Sbjct: 139 NDAGVYVLLVRLDHSRS-TDGFILGVNVY 166

□ >gi|9625941|ref|NP_040189.1| membrane glycoprotein I [Human herpesvirus 3]
 gi|138331|sp|P09258|VGLI_VZVD GLYCOPROTEIN I PRECURSOR (GLYCOPROTEIN IV) (GI) (GPI)
 gi|73744|pir||VGBE67 glycoprotein D precursor - human herpesvirus 3
 gi|59986|emb|CAA25032.1| unnamed protein product [Human herpesvirus 3]
 gi|60056|emb|CAA27950.1| unnamed protein product [Human herpesvirus 3]
 gi|7385040|gb|AAF61668.1| ORF67 [Human herpesvirus 3]
 gi|10697359|gb|AAG21703.1| ORF67 [Human herpesvirus 3 MSP]
 gi|11245957|gb|AAG32557.1| ORF67; gI [Human herpesvirus 3]
 gi|12232345|gb|AAG48519.1| glycoprotein I [Human herpesvirus 3]
 gi|12657832|gb|AAK01046.1| glycoprotein I [Human herpesvirus 3]
 gi|13400038|gb|AAK19945.1| ORF67 [Human herpesvirus 3]
 gi|13400054|gb|AAK19971.1| ORF67 [Human herpesvirus 3]
 gi|13400068|gb|AAK19962.1| ORF67 [Human herpesvirus 3]
 gi|13400084|gb|AAK19954.1| ORF67 [Human herpesvirus 3]
 gi|14017396|gb|AAK50451.1| glycoprotein I [Human herpesvirus 3 VZV-Ellen]
 gi|30575407|gb|AAP32833.1| glycoprotein I [Human herpesvirus 3]
 gi|30575418|gb|AAP32838.1| glycoprotein I [Human herpesvirus 3]
 gi|30575429|gb|AAP32843.1| glycoprotein I [Human herpesvirus 3]
 gi|30575440|gb|AAP32848.1| glycoprotein I [Human herpesvirus 3]
 gi|30575451|gb|AAP32853.1| glycoprotein I [Human herpesvirus 3]
 gi|30575462|gb|AAP32858.1| glycoprotein I [Human herpesvirus 3]
 gi|30575473|gb|AAP32863.1| glycoprotein I [Human herpesvirus 3]
 gi|30575482|gb|AAP32867.1| glycoprotein I [Human herpesvirus 3]
 Length = 354

Score = 55.8 bits (133), Expect = 1e-06
 Identities = 41/149 (27%), Positives = 72/149 (48%), Gaps = 9/149 (6%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPE---ATIQLQLFFMPGQRP HKP-YS GTVRVAFRSD 77
 ++ G+HVS +++ I+ P I+ QL F+ Q P YSGT+ + + +D
 Sbjct: 20 ALIFKGDHVS LQVNSSLTSILIPMQNDNYTEIKGQLVF IGEQLPTGTNYS GTLELLY-AD 78

Query: 78 ITNQCYQELSEERFENC THRSSSVFVGCKVTE---YTFSASNRLTGPPHPFKLTIRNPRP 134
 C++ + R++ C +S F+ C+ Y S T P L I P
 Sbjct: 79 TVAFCFRSVQVIRYDGCPRIRTSAFISCRYKHSWHYGNSTDRISTEPDAGV MLKITKPGI 138

Query: 135 NDSGMFYVIVRLDDTKEPIDVF AIQLSVY 163
 ND+G++ ++VRLD ++ D F + ++VY
 Sbjct: 139 NDAGVYVLLVRLDHSRS-TDGFILGVNVY 166

□ >gi|3724277|dbj|BAA33764.1| glycoprotein I [Canine herpesvirus]
 Length = 259

Score = 51.2 bits (121), Expect = 3e-05
Identities = 39/147 (26%), Positives = 67/147 (45%), Gaps = 8/147 (5%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPH-KPYSGTVRVAFRSDITN 80
G V G ++S ++ + P + + +L F+ Q YSGT+ N
Sbjct: 34 GFVYKGTIYISMFLNTSSGFSIFPDDKFIVSGRLLFLNDQHLNVNNYSGTIEFI---HFNN 90

Query: 81 QCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPNDSG 138
CY + +C ++ F C KV+++ S + + L I NP+PNDSG
Sbjct: 91 SCYTVYQTIEYFSCPRIFNNAFRSCLKKVKSHHESQLRINSSIENGVLLEITNPKPNDSG 150

Query: 139 MFYVIVRLDDTKEPIDVFAIQLSVYQF 165
++++ V+L++ K DVF I +Y F
Sbjct: 151 VYFIRVQLENNK--TDVFGIPAFIYSF 175

☐ >[gi|2337933|gb|AAB67059.1|](#) cUS7 [Canine herpesvirus]
[gi|3724279|dbj|BAA33765.1|](#) glycoprotein I [Canine herpesvirus]
[gi|13959013|gb|AAK51063.1|](#) glycoprotein I [Canine herpesvirus]
Length = 364

Score = 50.1 bits (118), Expect = 8e-05
Identities = 39/147 (26%), Positives = 67/147 (45%), Gaps = 8/147 (5%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPH-KPYSGTVRVAFRSDITN 80
G V G ++S ++ + P + + +L F+ Q YSGT+ N
Sbjct: 34 GFVYKGTIYISMFLNTSSGFSIFPDDKFIVSGRLLFLDDQHLNVNNYSGTIEFI---HFNN 90

Query: 81 QCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPNDSG 138
CY + +C ++ F C KV+++ S + + L I NP+PNDSG
Sbjct: 91 SCYTVYQTIEYFSCPRIFNNAFRSCLKKVKSHHESQLRINSSIENGVLLEITNPKPNDSG 150

Query: 139 MFYVIVRLDDTKEPIDVFAIQLSVYQF 165
++++ V+L++ K DVF I +Y F
Sbjct: 151 VYFIRVQLENNK--TDVFGIPAFIYSF 175

☐ >[gi|3777490|gb|AAC67213.1|](#) gI [Canine herpesvirus]
Length = 364

Score = 50.1 bits (118), Expect = 8e-05
Identities = 39/147 (26%), Positives = 67/147 (45%), Gaps = 8/147 (5%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPH-KPYSGTVRVAFRSDITN 80
G V G ++S ++ + P + + +L F+ Q YSGT+ N
Sbjct: 34 GFVYKGTIYISMFLNTSSGFSIFPDDKFIVSGRLLFLDDQHLNVNNYSGTIEFI---HFNN 90

Query: 81 QCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPNDSG 138
CY + +C ++ F C KV+++ S + + L I NP+PNDSG
Sbjct: 91 SCYTVYQTIEYFSCPRIFNNAFRSCLKKVKSHHESQLRINSSIENGVLLEITNPKPNDSG 150

Query: 139 MFYVIVRLDDTKEPIDVFAIQLSVYQF 165
++++ V+L++ K DVF I +Y F
Sbjct: 151 VYFIRVQLENNK--TDVFGIPAFIYSF 175

□ >[gi|15216212|emb|CAC51466.1|](#) glycoprotein I [Phocid herpesvirus 1]
Length = 369

Score = 50.1 bits (118), Expect = 9e-05

Identities = 42/148 (28%), Positives = 68/148 (45%), Gaps = 9/148 (6%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRP-EATIQQLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
GIV G ++S ++ V P + + L F+ QR P YSGT+ + +
Sbjct: 16 GIVYRGTYMSMYVNTSSGYTVYPDDRDFNVTGYLLFLDDQRLPVTNYSGTIEIIY---FN 72

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPND 137
CY + +C ++ F C KV+++ S + L I+NP+P+DS
Sbjct: 73 YSCYTVYQTIIEYVSCPRIHNNAFRSCLIKVSKHHQSQLRINSSIETGVLLLEIKNPKPSDS 132

Query: 138 GMFYVIVRLDDTKEPIDVFVFIQLSVYQF 165
G++ V+L++ K DVF I VY F
Sbjct: 133 GVIYIFRVQLENNK--TDVFGISAFVYSF 158

□ >[gi|632872|gb|AAB30981.1|](#) glycoprotein gI [Feline herpesvirus 1]
Length = 370

Score = 48.9 bits (115), Expect = 2e-04

Identities = 40/148 (27%), Positives = 69/148 (46%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEA-TIQQLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
GIV G+HVS +D ++ P E TI L F+ Q P Y+GT+ + +
Sbjct: 18 GIVYRGDHVSLHVDTSSTGFVIYPTLENFTIYGHLLIFLDDQPLPVNNYNGTLEI-IHYNHH 76

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPND 137
+ CY+ + + +C ++ F C K + + + + T LTI +P+ D
Sbjct: 77 SSCYKIVQVIEYSSCPVRNNAFRSCLHKTSMHQYDQLSINTSVETGMMLLTITSPKMEDG 136

Query: 138 GMFYVIVRLDDTKEPIDVFVFIQLSVYQF 165
G++ + VR + + DVF + + VY F
Sbjct: 137 GIYALRVRFNHNKKA-DVFGLSVFEVYSF 163

□ >[gi|893371|dbj|BAA44952.1|](#) homologue of HSV-1 gI [Feline herpesvirus 1]
Length = 384

Score = 48.5 bits (114), Expect = 2e-04

Identities = 40/148 (27%), Positives = 69/148 (46%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEA-TIQQLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
GIV G+HVS +D ++ P E TI L F+ Q P Y+GT+ + +
Sbjct: 18 GIVYRGDHVSLHVDTSSTGFVIYPTLENFTIYGHLLIFLDDQPLPVNNYNGTLEI-IHYNHH 76

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASNRLTGPPHPFKLTIRNPRPND 137
+ CY+ + + +C ++ F C K + + + + T LTI +P+ D
Sbjct: 77 SSCYKIVQVIEYSSCPVRNNAFRSCLHKTSMHQYDQLSINTSVETGMMLLTITSPKMEDG 136

Query: 138 GMFYVIVRLDDTKEPIDVFVFIQLSVYQF 165
G++ + VR + + DVF + + VY F
Sbjct: 137 GIYALRVRFNHNKKA-DVFGLSVFEVYSF 163

□>gi|1405557|emb|CAA67077.1| gI [Feline herpesvirus 1]
Length = 384

Score = 48.5 bits (114), Expect = 3e-04

Identities = 40/148 (27%), Positives = 69/148 (46%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEA-TIQLQLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
GIV G+HVS +D ++ P E TI L F+ Q P Y+GT+ + +
Sbjct: 18 GIVYRGDHVSLHVDTS SSGFVIYPTLENFTIYGHLLIFLDDQPLPVNNYNGTLEI-IHYNHH 76

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNPRPND 137
+ CY+ + + +C ++ F C K + + + + T LTI +P+ D
Sbjct: 77 SSCYKIVQVIEYSSCPVRNNAFRSCLHKTSMHQYDQLSINTSVETGMLLTITSPKMEDG 136

Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQF 165
G++ + VR + + DVF + + VY F
Sbjct: 137 GIYALRVRFNHNKA-DVFGLSVFEVYSF 163

□>gi|13242461|ref|NP_077481.1| glycoprotein I [Cercopithecine herpesvirus 7]
gi|549313|sp|Q04547|VGLI_CHV9D Glycoprotein I precursor (Membrane glycoprotein 1)
gi|423904|pir||C46113 glycoprotein D precursor - cercopithecine herpesvirus 9 (s
DHV)
gi|310718|gb|AAA47888.1| membrane glycoprotein
gi|11036613|gb|AAG27242.1| glycoprotein I [Cercopithecine herpesvirus 7]
Length = 353

Score = 46.2 bits (108), Expect = 0.001

Identities = 36/152 (23%), Positives = 71/152 (46%), Gaps = 6/152 (3%)

Query: 22 GIVITGNHVSARIDDD--HIVIVAPRPEATIQLQLFFMPGQRP-HKPYS GTVRVAFRSDI 78
I+ GN++S ++ I + +A+I+ + F+ Q P Y+ TV + +
Sbjct: 27 AIIYRGN YISLYVNSSATSIFLKGNNNDASIRGRFLFIGDQFPVTNTYNVTVEL-LHVNQ 85

Query: 79 TNQCYQELSEERFENCNTHRSSSVFVGCKVTE-YTFASASNRLTGPPHPFKLTIRNPRPND 137
T C Q L + C + + C+V + + + +LT P + N + D+
Sbjct: 86 TTLCLQPLYRVMYGECPRIRTGAIACRVKRSWHYENATQLTDPNVEIIFKMNNTKVEDA 145

Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQFANTA 169
G++ ++V+LD T D+F + L+VY +T+
Sbjct: 146 GIYLLVVQLDYT-SLFDIFFVSLNVYPKQDTS 176

□>gi|227760|prf||1710264F ORF 6
Length = 253

Score = 45.8 bits (107), Expect = 0.001

Identities = 36/128 (28%), Positives = 57/128 (44%), Gaps = 7/128 (5%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPE-ATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITNQ 81
IV TG V+ D +V + ++ QL F+ Q Y+GT + + D +
Sbjct: 19 IVYTGTSVTLSTDQSALVAFCGLDKMVNVRGQLLFLGDQTRTSSYTGTTEI-LKWDEEYK 77

Query: 82 CYQELSEERFENCNTHRSSSVFVGCKVTEYTFASASNRLTGPPHPFK--LTIRNPRPND 138
CY L + +C ++VF GC+ +R+ P P K L I PR +D+G
Sbjct: 78 CYSVLHATS YMDCPAIDATVFRGCRDAVVYAQPHDRVQ--PFPEKGTLLRIVEPRVSDTG 135

Query: 139 MFYVIVRL 146
+Y+ V L
Sbjct: 136 SYIIRVAL 143

□>[gi|10180781|gb|AAG14269.1|](#) US7 membrane glycoprotein I-like protein [Gallid her
[gi|22654926|gb|AAM97723.1|](#) glycoprotein I [Gallid herpesvirus 2]
[gi|41387572|gb|AAS01616.1|](#) glycoprotein I [Gallid herpesvirus 2]
Length = 355

Score = 45.4 bits (106), Expect = 0.002
Identities = 36/128 (28%), Positives = 57/128 (44%), Gaps = 7/128 (5%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPE-ATIQQLFFMPGQRPHKPYSGTVRVAFRSDITNQ 81
IV TG V+ D +V + ++ QL F+ Q Y+GT + + D +
Sbjct: 19 IVYTGTSTVLSTDQSAALVAFCLDKMVNVRGQLLEFLGDQTRTSSYTGTTEI-LKWDEEYK 77

Query: 82 CYQELSEERFENCNTHRSSSVFVGCKVTEYTFASASNRLTGPPHPFK---LTIRNPRENDSG 138
CY L + +C ++VF GC+ +R+ P P K L I PR +D+G
Sbjct: 78 CYSVLHATSYMDCPAIDATVFRGCRDAVVYAQPHDRVQ--PFPEKGTLLRIVEPRVSDTG 135

Query: 139 MFYVIVRL 146
+Y+ V L
Sbjct: 136 SYIIRVAL 143

□>[gi|12084907|ref|NP_073377.1|](#) US7 membrane glycoprotein I [Meleagrid herpesvirus
[gi|543548|pir||JQ2352](#) glycoprotein I - turkey herpesvirus
[gi|406790|emb|CAA48618.1|](#) glycoprotein homologue I [Gallid herpesvirus 2]
[gi|11095904|gb|AAG30111.1|](#) US7 glycoprotein gI precursor [Meleagrid herpesvirus 1]
[gi|12025190|gb|AAG45816.1|](#) US7 membrane glycoprotein I [Meleagrid herpesvirus 1]
Length = 356

Score = 45.1 bits (105), Expect = 0.003
Identities = 36/127 (28%), Positives = 57/127 (44%), Gaps = 3/127 (2%)

Query: 23 IVITGNHVSARIDDD-HIVIVAPRPEATIQQLFFMPGQRPHKPYSGTVRVAFRSDITNQ 81
+V G+ VS +D I + ++ FM Q + YSGT+ + + + N+
Sbjct: 26 MVYRGLSVSTTVDSQAIAFFGIDTVNLYGKVLFGMDQYLEEIYSGTMEI-LKWNQANR 84

Query: 82 CYQELSEERFENCNTHRSSSVFVGCK-VTEYTFASASNRLTGPPHPFKLTIRNPRPNDSGMF 140
CY + +C SS+VF GC+ YT S + LTI PR DSG++
Sbjct: 85 CYSIAHATYYADCPIISSTVFRGCRDAVVYTRPHSRIHPQYRNGLLLTIIIEPRMEDSGIY 144

Query: 141 YVIVRLD 147
Y+ +D
Sbjct: 145 YIRTSID 151

□>[gi|765053|gb|AAA64968.1|](#) membrane glycoprotein I
[gi|22654934|gb|AAM97727.1|](#) glycoprotein I [Gallid herpesvirus 2]
Length = 355

Score = 44.7 bits (104), Expect = 0.004
Identities = 38/130 (29%), Positives = 58/130 (44%), Gaps = 11/130 (8%)

Query: 23 IVITGNHVSARIDDDHIVIVAPR---PEATIQLQLFFMPGQRPHPYSGTVRVAFRSDIT 79
 IV TG V+ + D +VA R ++ QL F+ Q Y+GT + + D
 Sbjct: 19 IVYTGTSVT--LSTDQSALVAFRGLDKMVNVRGQLLFLGDQTRTSSYTGTTEI-LKWDEE 75

Query: 80 NQCYQELSEERFENCTHRSSSVFVGCKVTEYTFASASNRLTGPPHPFK---LTIRNRPND 136
 +CY L + +C ++VF GC+ R+ P P K L I PR +D
 Sbjct: 76 YKCYSVLHATS YMDCPAIDATVFRGCRDAVVYAQPHGRVQ--PFPEKGTLLRIVEPRVSD 133

Query: 137 SGMFYVIVRL 146
 +G +Y+ V L
 Sbjct: 134 TGSYYIRVSL 143

☐ >[gi|42795204|gb|AAS45961.1|](#) envelope glycoprotein I [Equine herpesvirus 1]
 Length = 424

Score = 44.7 bits (104), Expect = 0.004
 Identities = 37/148 (25%), Positives = 65/148 (43%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQR-PHPYSGTVRVAFRSDIT 79
 I+ G H+S ++ V P ++ + + L F+ GQR P YSG + + + +
 Sbjct: 22 AIIYRGEHMSMYLNASSEFAVYPTDQSLVLVGHLLFLDGQRLPTTNYSGLIEL-IHYNYS 80

Query: 80 NQCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNRPND 137
 + CY + +E+C +++ F C K +++ L I P+P DS
 Sbjct: 81 SVCYTVIQTISYESCPRVANNAFRSCLHKTSKHYHDYFRVNVSVETNVLLNITKPQPTDS 140

Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQF 165
 G + + V+LD DVF + VY
 Sbjct: 141 GAYILRVKLDHAPTA-DVFGVSAFVYDL 167

☐ >[gi|9626810|ref|NP_041082.1|](#) membrane glycoprotein I [Equine herpesvirus 1]
[gi|138329|sp|P18553|VGLI_EHV1B](#) Glycoprotein I precursor
[gi|73784|pir||VGBEE9](#) glycoprotein gp63 precursor - equine herpesvirus 1
[gi|330788|gb|AAA66547.1|](#) glycoprotein I
[gi|330864|gb|AAB02508.1|](#) membrane glycoprotein I
 Length = 424

Score = 44.7 bits (104), Expect = 0.004
 Identities = 37/148 (25%), Positives = 65/148 (43%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQR-PHPYSGTVRVAFRSDIT 79
 I+ G H+S ++ V P ++ + + L F+ GQR P YSG + + + +
 Sbjct: 22 AIIYRGEHMSMYLNASSEFAVYPTDQSLVLVGHLLFLDGQRLPTTNYSGLIEL-IHYNYS 80

Query: 80 NQCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNRPND 137
 + CY + +E+C +++ F C K +++ L I P+P DS
 Sbjct: 81 SVCYTVIQTISYESCPRVANNAFRSCLHKTSKHYHDYFRVNASVETNVLLNITKPQPTDS 140

Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQF 165
 G + + V+LD DVF + VY
 Sbjct: 141 GAYILRVKLDHAPTA-DVFGVSAFVYDL 167

□ >gi|40787939|ref|NP_954960.1| US7 glycoprotein I [Bovine herpesvirus 5]
gi|40456196|gb|AAR86174.1| US7 glycoprotein I [Bovine herpesvirus 5]
Length = 387

Score = 44.7 bits (104), Expect = 0.004
Identities = 43/153 (28%), Positives = 67/153 (43%), Gaps = 11/153 (7%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQ--LFFMPGQRPH-KPYSGTVRVAFRSDI 78
G+V G V R D V P +AT+ L+ L F+ Q P + Y+GTV + R +
Sbjct: 21 GLVYRGEAVGLRADGPVAFVHP-ADATLALRGRLIFLEHQLPAGRRYNGTVEL-LRYLV 78

Query: 79 TNQCYQELSEERFENCTHRSSSVFVGCKVTEYTFASASNRLTGPP--HPFKLTIRNPRPND 136
C+ L F +C ++ F C + + S R + +I PRP D
Sbjct: 79 DGDCFVMLQATAFASCPRVANDAFRSCLHADTRPARSERRVSAAVENHVLFSIAGPRPAD 138

Query: 137 SGMFYVIVRLDDTKEPI-----DVFAIQLSVYQF 165
SG++++ V +D E DVF + V+ F
Sbjct: 139 SGLYFLRVGIDGGAEGAERRRDVFPLAAFVHGF 171

□ >gi|42566423|gb|AAS21042.1| glycoprotein I [Bovine herpesvirus 5 strain TX89]
Length = 387

Score = 44.7 bits (104), Expect = 0.004
Identities = 43/153 (28%), Positives = 67/153 (43%), Gaps = 11/153 (7%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQ--LFFMPGQRPH-KPYSGTVRVAFRSDI 78
G+V G V R D V P +AT+ L+ L F+ Q P + Y+GTV + R +
Sbjct: 21 GLVYRGEAVGLRADGPVAFVHP-ADATLALRGRLIFLEHQLPAGRRYNGTVEL-LRYLV 78

Query: 79 TNQCYQELSEERFENCTHRSSSVFVGCKVTEYTFASASNRLTGPP--HPFKLTIRNPRPND 136
C+ L F +C ++ F C + + S R + +I PRP D
Sbjct: 79 DGDCFVMLQATAFASCPRVANDAFRSCLHADTRPARSERRVSAAVENHVLFSIAGPRPAD 138

Query: 137 SGMFYVIVRLDDTKEPI-----DVFAIQLSVYQF 165
SG++++ V +D E DVF + V+ F
Sbjct: 139 SGLYFLRVGIDGGAEGAERRRDVFPLAAFVHGF 171

□ >gi|22654930|gb|AAM97725.1| glycoprotein I [Gallid herpesvirus 2]
Length = 355

Score = 43.9 bits (102), Expect = 0.006
Identities = 36/128 (28%), Positives = 56/128 (43%), Gaps = 7/128 (5%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQRPHKPYSCTVRVAFRSDITNQ 81
IV TG V+ D +V + + QL F+ Q Y+GT + + D +
Sbjct: 19 IVYTGTSVTLSTDQSAFVAFGLDKMVNERGQLLFLGDQTRTSSYTGTTEI-LKWDEEYK 77

Query: 82 CYQELSEERFENCTHRSSSVFVGCKVTEYTFASASNRLTGPPHPFK---LTIRNPRPNDSDG 138
CY L + +C ++VF GC+ +R+ P P K L I PR +D+G
Sbjct: 78 CYSVLHATSMDCPAIDATVFRGCRDAVVYAQPHDRVQ--PFPEKGTLLRIVEPRVSDTG 135

Query: 139 MFYVIVRL 146
+Y+ V L
Sbjct: 136 SYIIRVAL 143

□ >gi|22654932|gb|AAM97726.1| glycoprotein I [Gallid herpesvirus 2]
Length = 355

Score = 43.9 bits (102), Expect = 0.007

Identities = 35/127 (27%), Positives = 56/127 (44%), Gaps = 7/127 (5%)

Query: 24 VITGNHVSARIDDDHIVIVAPRPE-ATIQLQLFFMPGQRPHKPYSGTVRVAFRSDITNQC 82
V TG V+ D +V + ++ QL F+ Q Y+GT + + D +C
Sbjct: 20 VYTGTSVTLSTDQSALVAFCLDKMNVNRGQLLFLGDQTRTSSYTGTTEI-LKWDEEYKC 78

Query: 83 YQELSEERFENCNTHRSSSVFVGCKVTEYTFASASNRLTGPPHPFK---LTIRNPRPNDSGM 139
Y L + +C ++VF GC+ +R+ P P K L I PR +D+G
Sbjct: 79 YSVLHATSYMDCPAIDATVFRGCRDAVVYAQPHDRVQ--PFPEKGTLLRIVEPRVSDTGS 136

Query: 140 FYVIVRL 146
+Y+ V L
Sbjct: 137 YYIRVAL 143

□ >gi|9629803|ref|NP_045290.1| 73 [Equine herpesvirus 4]
gi|11278216|pir||T42616 envelope protein - equine herpesvirus 4 (strain NS80567)
gi|2606021|gb|AAC59593.1| 73 [Equine herpesvirus 4]
Length = 420

Score = 43.1 bits (100), Expect = 0.009

Identities = 36/148 (24%), Positives = 66/148 (44%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
I+ G H+S ++ V P+ ++ + + + F+ GQR P YSG + + + +
Sbjct: 22 AIIYRGEHMSMYLNASSEFAVYPKDKSLVVVGHMLFLDGQRLPTTNYSGLIEL-IHHNYS 80

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNPRPNDS 137
CY + +E+C +++ F C K + + + T L I P+P DS
Sbjct: 81 RGCYSVIQTISYESCPRVANNAFRSCLHKTSNHNQDYFHVNTSVETNVLLNITRPQPADS 140

Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQF 165
G + + V+L+ DVF + VY
Sbjct: 141 GAYILRVKLNHAPTA-DVFGVSAFVYDL 167

□ >gi|625559|pir||A61162 glycoprotein I - equine herpesvirus 1 (strain Abl) (frag
Length = 149

Score = 42.7 bits (99), Expect = 0.013

Identities = 32/130 (24%), Positives = 59/130 (45%), Gaps = 5/130 (3%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
I+ G H+S ++ V P ++ + + L F+ GQR P YSG + + + +
Sbjct: 14 AIIYRGGHMSMYLNASSEFAVYPTDQSLVLVGHLFLDGQRLPTTNYSGLIEL-IHYNYS 72

Query: 80 NQCYQELSEERFENCNTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNPRPNDS 137
+ CY + +E+C +++ F C K +++ L I P+P DS
Sbjct: 73 SVCYTVIQTISYESCPRVANNAFRSCLHKTSKHYHDYFRVNASVETNVLLNITKPQPTDS 132

Query: 138 GMFYVIVRLD 147

G + + V+LD
Sbjct: 133 GAYILRVKLD 142

□ >[gi|2924616|dbj|BAA25021.1|](#) glycoprotein I homologue [Equine herpesvirus 4]
Length = 420

Score = 42.0 bits (97), Expect = 0.022
Identities = 36/148 (24%), Positives = 66/148 (44%), Gaps = 6/148 (4%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQL-QLFFMPGQR-PHKPYSGTVRVAFRSDIT 79
I+ G H+S ++ V P+ ++ + + + F+ GQR P YSG + + + +
Sbjct: 22 AIIYRGEHMSMYLNASSEFAVYPKDKSLVVVGHMLFLDGQRLPTTNYSGLIEL-IHNNYS 80
Query: 80 NQCYQELSEERFENCTHRSSSVFVGC--KVTEYTFASASNRLTGPPHPFKLTIRNPRPND 137
CY + +E+C +++ F C K + + + T L I P+P DS
Sbjct: 81 RGCYSVIQTISYESCPRVANNAFRSCLHKTSNHNQDYFHVNTSVETNVLLNITWQPADS 140
Query: 138 GMFYVIVRLDDTKEPIDVFAIQLSVYQF 165
G + + V+L+ DVF + VY
Sbjct: 141 GAYILRVKLNHAPTA-DVFGVSAFVYDL 167

□ >[gi|22654928|gb|AAM97724.1|](#) glycoprotein I [Gallid herpesvirus 2]
Length = 355

Score = 41.2 bits (95), Expect = 0.043
Identities = 34/130 (26%), Positives = 55/130 (42%), Gaps = 11/130 (8%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPE-ATIQLQLFFMPGQRPHKPYSCTVRVAFRSDITNQ 81
IV TG V+ D +V + ++ L F+ Q Y+GT + + D +
Sbjct: 19 IVYTGTSTLSTDQSALVAFCLDKMVNVRGLLLFLGDQTRTSSYTGTTEI-LKWDEEYK 77
Query: 82 CYQELSEERFENCTHRSSSVFVGCQVTEYTFASASNRLTGPPHPFK-----LTIRNPRPND 136
CY L + +C ++VF GC+ +R+ PF L I PR +D
Sbjct: 78 CYSVLHATSYMDCPAIDATVFRGCRDAVVYAQPHDRV----QPFSEKGTLLRIVEPRVSD 133
Query: 137 SGMFYVIVRL 146
+G +Y+ V L
Sbjct: 134 TGSYYIRVAL 143

□ >[gi|10834952|ref|NP_066913.1|](#) glycoprotein I [Gallid herpesvirus 3]
[gi|1339906|dbj|BAA12814.1|](#) glycoprotein homolog I [Gallid herpesvirus 1]
[gi|3374483|dbj|BAA32012.1|](#) glycoprotein I [Gallid herpesvirus 1]
[gi|10800046|dbj|BAB16591.1|](#) glycoprotein I [Gallid herpesvirus 3]
Length = 355

Score = 38.9 bits (89), Expect = 0.19
Identities = 34/142 (23%), Positives = 61/142 (42%), Gaps = 4/142 (2%)

Query: 23 IVITGNHVSARIDDDHIV-IVAPRPEATIQLQLFFMPGQRPHKPYSCTVRVAFRSDITNQ 81
++ TG +SA D IV + +LFF+ Y GT + R + +
Sbjct: 32 LIFTGTSLASTDQSAIVAFCLDKTVNVYGRLLFLGDSVGVISYDGTTEI-LRWNEKLK 90
Query: 82 CYQELSEERFENCTHRSSSVFVGCQVTEYTFASASNRLTGPPHP-FKLTIRNPRPNDSGMF 140

C+ + + +C S++F GC+ + +R+ L I +PR +D+G +
Sbjct: 91 CFSVMYAALYTDCPLAGSALFRGCRSAVVYATPHDRVKPVSEKGLLLCISDPRI SDTGT Y 150

Query: 141 YVIVRLDDTKEPIDVFAIQLSV 162
Y+ V L + D+F I + V
Sbjct: 151 YIRVSLAG-RNVSDIFRIDVVV 171

□ >gi|138330|sp|P07646|VGLI_PRVRI GLYCOPROTEIN GP63 PRECURSOR
gi|73783|pir||VGBE63 glycoprotein gp63 - suid herpesvirus 1
gi|334056|gb|AAC35204.1| gp63 glycoprotein [Pseudorabies virus]
Length = 350

Score = 38.9 bits (89), Expect = 0.21
Identities = 32/131 (24%), Positives = 52/131 (39%), Gaps = 5/131 (3%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITNQ 81
G++ G VS + +++ P TI L F+ G P YSG V + R D
Sbjct: 31 GVLFRGAGVSVHVAGSAVLVPGDAPNLTIDGTLFLFEGPSPSN-YSGRVEL-LRLDPKRA 88
Query: 82 CYQELSEERFENC THRSSSVFVGCKVTEYTF SASNRLTGPPHPFKLT-IRNPRPNDSGMF 140
CY ++ C F GC + R + +L + P P D+G +
Sbjct: 89 CYTREYAAEYDLCPRVHHEAFRGCLR KREPLA--RRASA AVEARRLLFVSRPAPPDAGSY 146
Query: 141 YVIVRLDDTKE 151
+ VR++ T +
Sbjct: 147 VLRVRVNGTTD 157

□ >gi|40254013|tpg|DAA02208.1| TPA: membrane glycoprotein gI precursor [Suid herpe
Length = 366

Score = 38.9 bits (89), Expect = 0.21
Identities = 32/131 (24%), Positives = 52/131 (39%), Gaps = 5/131 (3%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITNQ 81
G++ G VS + +++ P TI L F+ G P YSG V + R D
Sbjct: 31 GVLFRGAGVSVHVAGSAVLVPGDAPNLTIDGTLFLFEGPSPSN-YSGRVEL-LRLDPKRA 88
Query: 82 CYQELSEERFENC THRSSSVFVGCKVTEYTF SASNRLTGPPHPFKLT-IRNPRPNDSGMF 140
CY ++ C F GC + R + +L + P P D+G +
Sbjct: 89 CYTREYAAEYDLCPRVHHEAFRGCLR KREPLA--RRASA AVEARRLLFVSRPAPPDAGSY 146
Query: 141 YVIVRLDDTKE 151
+ VR++ T +
Sbjct: 147 VLRVRVNGTTD 157

□ >gi|37576286|gb|AAQ86799.1| membrane glycoprotein gI [Suid herpesvirus 1]
Length = 366

Score = 38.9 bits (89), Expect = 0.21
Identities = 32/131 (24%), Positives = 52/131 (39%), Gaps = 5/131 (3%)

Query: 22 GIVITGNHVSARIDDDHIVIVAPRPEATIQLQLFFMPGQRPHKPYS GTVRVAFRSDITNQ 81
G++ G VS + +++ P TI L F+ G P YSG V + R D

Sbjct: 31 GVLFRGAGVSVHVAGSAVLVPGDAPNLTIDGTLLFLEGPSPSN-YSGRVEL-LRLDPKRA 88

Query: 82 CYQELSEERFENCTHRSSSVFVGCKVTEYTFESASNRLTGPPHPFKLT-IRNPRPNDSGMF 140
 CY ++ C F GC + R + +L + P P D+G +

Sbjct: 89 CYTREYAAEYDLCPRVHHEAFRGCLRKREPLA--RRASAAVEARRLLFVSRPAPPDAGSY 146

Query: 141 YVIVRLDDTKE 151
 + VR++ T +

Sbjct: 147 VLRVRVNGTTD 157

☐ >gi|9629887|ref|NP_045371.1| glycoprotein I [Bovine herpesvirus 1]
 gi|2653360|emb|CAA06146.1| glycoprotein I [Bovine herpesvirus type 1.1 (strain Coe)]
 gi|3355725|emb|CAB10890.1| glycoprotein I [Bovine herpesvirus 1]
 Length = 382

Score = 37.0 bits (84), Expect = 0.78
 Identities = 40/153 (26%), Positives = 66/153 (43%), Gaps = 11/153 (7%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPEATIQLQ--LFFMPGQRPK-KPYSGTVRVAFRSDIT 79
 +V G V R D V P +AT+ L+ L F+ Q P + Y+GTV + R

Sbjct: 21 LVYRGEAVGLRADGPVAFVHP-TDATLALRGRILFLEHQLPAGRRYNGTVEL-LRYHAA 78

Query: 80 NQCYQELSEERFENCTHRSSSVFVGCKVTEYTFESASNRLTGPP--HPFKLTIRNPRPNDS 137
 C+ L F +C ++ F C + + S R + +I +PRP DS

Sbjct: 79 GDCFVMLQTTAFASCPRVANDAFRSCLHADTRPARSERRASAAVENHVLFSIAHPRPIDS 138

Query: 138 GMFYVIVRL----DDTKEPIDVFVFIQLSVYQFA 166
 G++++ V + ++ DVF + V+ F

Sbjct: 139 GLYFLRVGIYGGTAGSERRRDVFPLAAVHVSFG 171

☐ >gi|1174955|sp|Q08102|VGLI_BHV1S Glycoprotein I
 gi|420427|pir||S35785 glycoprotein I - bovine herpesvirus 1
 gi|312189|emb|CAA80605.1| glycoprotein I [Bovine herpesvirus 1]
 Length = 380

Score = 36.6 bits (83), Expect = 1.0
 Identities = 40/153 (26%), Positives = 66/153 (43%), Gaps = 11/153 (7%)

Query: 23 IVITGNHVSARIDDDHIVIVAPRPEATIQLQ--LFFMPGQRPK-KPYSGTVRVAFRSDIT 79
 +V G V R D V P +AT+ L+ L F+ Q P + Y+GTV + R

Sbjct: 21 LVYRGEAVGLRADGPVAFVHP-TDATLALRGRILFLEHQLPAGRRYNGTVEL-LRYHAA 78

Query: 80 NQCYQELSEERFENCTHRSSSVFVGCKVTEYTFESASNRLTGPP--HPFKLTIRNPRPNDS 137
 C+ L F +C +++ F C + + S R + +I PRP DS

Sbjct: 79 GDCFVMLQTTAFASCPRVANNAFRSCLHADTRPARSERRASAAVENHVLFSIARPRPIDS 138

Query: 138 GMFYVIVRL----DDTKEPIDVFVFIQLSVYQFA 166
 G++++ V + ++ DVF + V+ F

Sbjct: 139 GLYFLRVGIYGGTAGSERRRDVFPLAAVHVSFG 171

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 1, 2004 2:20 AM
Number of letters in database: 760,540,814
Number of sequences in database: 2,727,393

Lambda	K	H
0.319	0.133	0.393

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 46,381,369

Number of Sequences: 2727393

Number of extensions: 1657189

Number of successful extensions: 3843

Number of sequences better than 10.0: 9

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 9

Number of HSP's that attempted gapping in prelim test: 3843

Number of HSP's gapped (non-prelim): 9

length of query: 362

length of database: 760,540,814

effective HSP length: 127

effective length of query: 235

effective length of database: 414,161,903

effective search space: 97328047205

effective search space used: 97328047205

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.8 bits)

S2: 75 (33.5 bits)